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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Curtis, Rory A.J.

Serial No.: 09/587,111

Filed: June 2, 2000

For: NOVEL MEMBERS OF THE
CAPSAICIN/VANILLOID RECEPTOR FAMILY OF
PROTEINS AND USES THEREOF

Attorney Docket No.: MNI-062CP2DV1

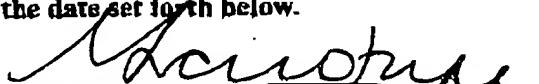
Group Art Unit: 1646

Examiner: Ulm, J. D.

Commissioner for Patents
Box AF
Washington, D.C. 20231Certificate of Facsimile TransmissionI hereby certify that this correspondence is being facsimile transmitted to the Commissioner for Patents,
Box AF, Washington, D.C. 20231 on the date set forth below.

By:

4/11/03


Maria Laccarripe Zacharakis, Ph.D.
Attorney for Applicant
Limited Recognition Under 37 C.F.R. 10.9(b)

Date of Signature

DECLARATION PURSUANT TO 37 CFR 81.131

Dear Sir:

I, Rory A.J. Curtis, a citizen of the United Kingdom, residing at 78 Hardwick Road,
Ashland, Massachusetts 01721 hereby declare as follows:

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Group Art Unit: 1646

(1) I am the inventor of the subject matter described and claimed in the above-identified application.

(2) Prior to January 22, 1999, the invention described and claimed in the above-referenced patent application was completed in this country, as evidenced by the following:

(a) Prior to January 22, 1999 I had completed the sequencing of the full length human VR-2 (SEQ ID NO:5) as evidenced by copies of the assembled contig map and the complete sequence of SEQ ID NO:5 derived from the contig map. The contig map and sequence print-out are submitted herewith as Exhibits A and B, respectively.

(b) Prior to January 22, 1999 I had determined that the polypeptide of SEQ ID NO:5 was a vanilloid receptor based on the results of a blast search using the amino acid sequence of SEQ ID NO:5. The top hit in this blast search analysis is rat vanilloid receptor 1 (VR-1; accession number AF029510). Based on the percent identity and percent similarity between the polypeptide of SEQ ID NO:5 and rat VR-1, and the fact that rat VR-1 was the top hit in the blast search analysis I determined that the polypeptide of SEQ ID NO:5 was a vanilloid receptor. The results of the blast search analysis are submitted herewith as Exhibit C.

(c) Prior to January 22, 1999, I had determined that the polypeptide of SEQ ID NO:5 represents a unique target for pain and that it may be responsible for hypersensitivity in chronic neuropathic pain, as evidenced by a copy of the "Qualified Target Summary Sheet" generated for this molecule. The Qualified Target Summary Sheet is submitted herewith as Exhibit D.

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(d) According to my routine practice, immediately after identifying the polypeptide of SEQ ID NO:5 as a vanilloid receptor (hVR-2) associated with pain and classifying it as a Qualified Target, I contemplated routine uses of this molecule such as: (i) use of the molecule in screening assays to identify modulators of the vanilloid receptor or (ii) use of this molecule in the diagnosis of conditions/diseases associated with, for example, aberrant vanilloid receptor (hVR-2) nucleic acid expression or activity, e.g., pain disorders, as evidenced by a copy of the "Qualified Target Summary Sheet" generated for this molecule.

(e) The dates deleted from the contig map (Exhibit A), the sequence print-out (Exhibit B), the blast search results (Exhibit C), and the Qualified Target Summary (Exhibit D) are prior to January 22, 1999.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this Application for Patent or any patent issuing thereon.

Rory Curtis
Rory A.J. Curtis, Ph.D.

4/10/2003
Date

Exhibit A

21ella
Sequencher™ "21ellaracefinal"

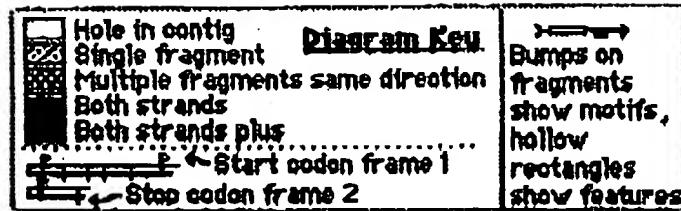
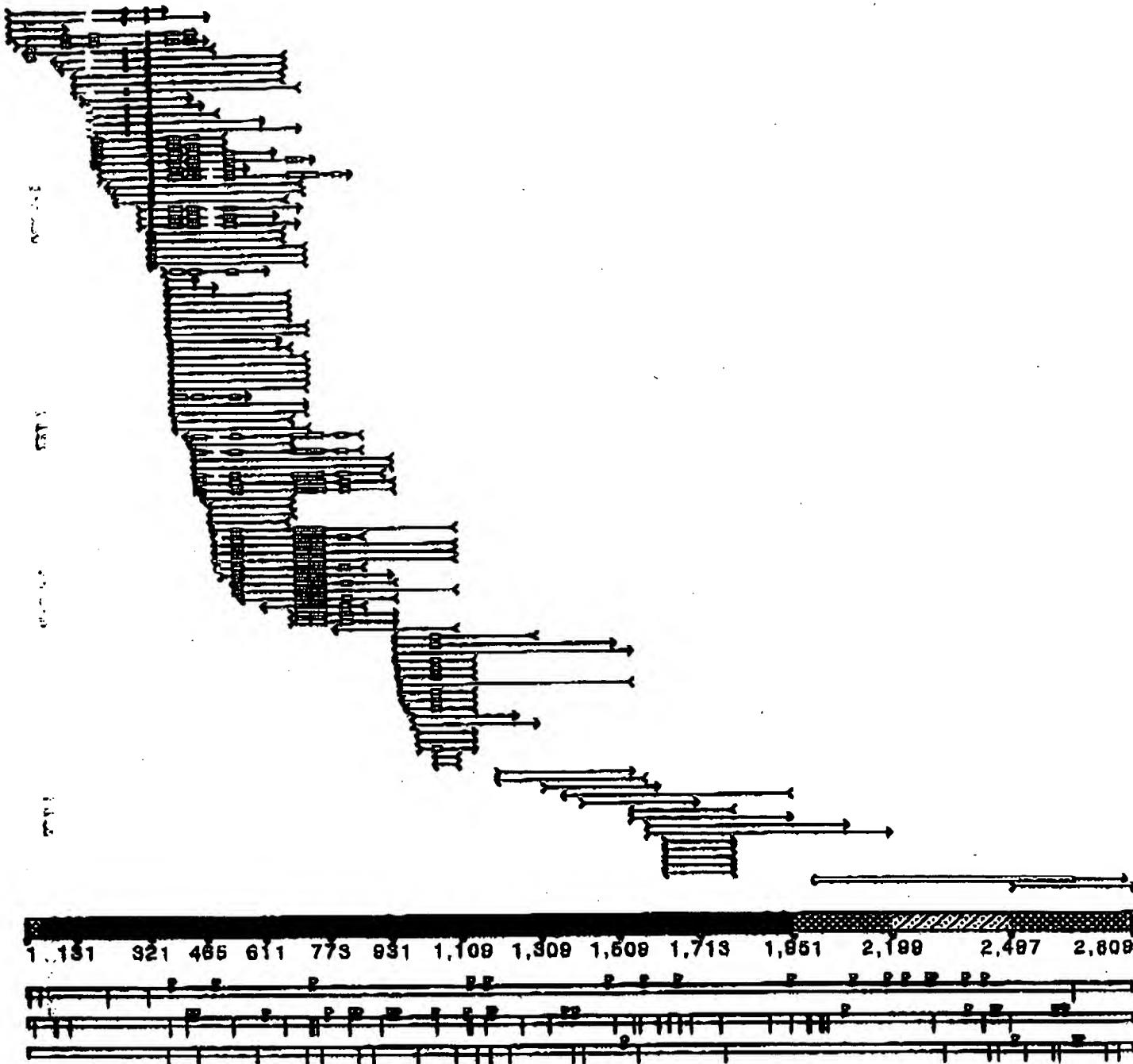


Exhibit B

21ella
Sequencher™ "21ellracefinal"

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Sequencer™ "21ellracefinal"

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flhx21el1z1	#71	ACCGACGCGC AGCTGGGAGG AAGACAGGAC CCTTGACATC TCCATCTGCA CAAAGTCCCT GGCTGGACCC AGCAGCTTC TCTCTCTAGG
Gseqbank H26..	#70	ACCGACGCGC A:NTGGGAGG AAGACAGGAC CCTTGACATC TCCATCTGCA CAGAGGTCCCT GGCTQQACGA NGCAGGCTCC TCCCTCC G
Gseqbank H29..	#257	ACCGACGCGC A:NTGGGAGG AAGACAGGAC CCTTGACATC TCCATCTGCA CAGAGGTCCCT GGCTQQACCO AGCAGGCTCC TCCCTCC G
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flhx21el1h1	#70	ACCGACGCGC AGTTGGHGG ANGACAGGAC CCTTGACATC TCCATCTGCA CAGAGGTCCCT AGCTQQACCO AGCAGGCTTC TCCCTCTAGG
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jchm103e2z2	#62	ACCGACGCGC AGCTGGGAGG AAGACAGGAC CCTTGACATC TCCATCTGCA CAGAGGTCCCT AGCTQQACCO AGCAGGCTCC TCCCTCC G
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jchm103e0c1..	#50	ACCGACGCGC AGCTGGGAGG AAGACAGGAC CCTTGACATC TCCATCTGCA CAGAGGTCCCT GGCTQQACCO AGCAGGCTCC TCCCTCC G
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Sequencher™ "21elli1racefinal"

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Sequencher™ "21ellracefinal"

18

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Zelella
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 | jcrn103-2x1 -> 94 NGAAAGGGAA CAGGTGCCA TCACCCGAT CCACCCGAT TTGACCGAGA TCGGCTCTTC ATTCGGTCT CCCGGGGGTGT CCCCCGGGAT
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Sequencer "21ellaracefinal"

Sequencher™ "21ella" racefinal"

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Sequencher™ "21elltracefinal"

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21ella
Sequencer "21ellracefinal"

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21el1a
Sequencher™ "21el1racefinal"

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fmkxlellr1- 8138	ACTGACTCCC AGGGCAACAC AGTCTCTGCAT GCCTTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
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2lella
Sequencher™ "2lellracefinal"

ftdab012c043.. #231 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 ftdab012c043.. #231 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 ftdab012c043.. #231 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 ftdab012c043.. #223 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 Genbank AA9.. #189 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 Genbank AA9.. #189 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 JBLAQ2910L.. >#1> GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 Genbank W38.. >#1>

f1171 GATGGGCTCC TCCAAAGCTGG GACCCGGCTC TGCCCTACCG TGAGCTTGA GGACATCCGC AACCTTCAGG ATCTCACGCC TCTGAAAGCTG
 D G L L Q A G A R L C P T V Q L E D I R N L Q D L T P L X L

ftdab012c043.. #321 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCA
 ftdab012c043.. #321 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 ftdab012c043.. #321 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 ftdab012c043.. #313 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 Genbank AA9.. #279 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 JBLAQ2910L.. #67 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 Genbank W38.. #65 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 Genbank AA9.. >#1>

f1261 ACCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAAGCGGGAA GTTTTCAGGA CTGAGCCACC TTTCGGAAA GTTCACCGAG
 A A K B G E I E I P R H I L Q R E Y S G L S H L S R K P T E

ftdab012c043.. #411 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 ftdab012c043.. #411 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 ftdab012c043.. #403 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 JBLAQ2910L.. #357 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 Genbank W38.. #255 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 Genbank AA9.. #366 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 ftdab012c043.. >#1> GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 Genbank AA9.. >#1>

f1351 TGGTCTATA GGCCTGTCCG GGTGTCTCG TATGACCTGG CTTCTGTGGA CAGCTGTCAQ GAGAACTCAQ TCTGGAGAT CATTGGCTTT
 H C Y G P V R V S L Y D L A S V D S C S E N S V L E I I A P

ftdab012c043.. #501 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG C
 ftdab012c043.. #501 CATTGCAAGA ACCCGAACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 ftdab012c043.. #493 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 JBLAQ2910L.. #367 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 Genbank W38.. #265 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 Genbank AA9.. #128 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 ftdab012c043.. #51 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 Genbank W38.. #51 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG

#1461 CATTGCAAGA GCCCCGACCG ACACCGAATG GTCGTTTGQ AGCCCCCTGAA CAAACTCTG CAGCGAAAT GGGATCTGCT CATCCCCAAG
 H C K S P H R M R M V V L E P L N K L L Q A K N D L L I P E

21ella
Sequencher™ "21ellatracefinal"

21ella - #425 GGCACTAAGC CAGATGGCAG CCCGGATGAG CGCTGGTGGT TCAAGGGTCAA GGAGGTGAAAC TGGGGCTTCAT GGGAGGAGAC GCTGCCCTACG
21ella - #431 TGAT GGGAGGAGAC GCTGCCCTACG

21ella - #2431 GGCACTAAGC CAGATGGCAG CCCGGATGAG CGCTGGTGGT TCAAGGGTCAA GGAGGTGAAAC TGGGGCTTCAT GGGAGGAGAC GCTGCCCTACG
G T K Y D G S P D S R H C P A V E S V N W A S W S Q T L P T

21ella - #515 CTCTGTGAGG ACCCGTCAGG GCCAAGGTCTC CCTCGAACTC TCGAGAAACCC TGTCTCTGGCT TCCCCCTCCA AGGAGGATGA GGATGGTGCC
21ella - #25 CTGTGTGAGG ACCCGTCAGG GCCAAGGTCTC CCTCGAACTC TCGAGAAACCC TGTCTCTGGCT TCCCCCTCCA AGGAGGATGA GGATGGTGCC

21ella - #2521 CTGTGTGAGG ACCCGTCAGG GCCAAGGTCTC CCTCGAACTC TCGAGAAACCC TGTCTCTGGCT TCCCCCTCCA AGGAGGATGA GGATGGTGCC
L C E D P S G A G V F R T L B N P V L A S P P K E D S D G A

21ella - #605 TCTGAGGAAA ACTATGTGCC CGTCCAGCTC CTCCAGTCCA ACTGATGGCC CAGATGCAAC AGGAGGGCCAG AGGACAGAGC AGAGGATCTT
21ella - #115 TCTGAGGAAA ACTATGTGCC CGTCCAGCTC CTCCAGTCCA ACTGATGGCC CAGATGCAAC AGGAGGGCCAG AGGACAGAGC ANAGGATCTT

21ella - #2611 TCTGAGGAAA ACTATGTGCC CGTCCAGCTC CTCCAGTCCA ACTGATGGCC CAGATGCAAC AGGAGGGCCAG AGGACAGAGC AGAGGATCTT
S E N Y V F V Q L L Q S N . W D R C S R R P E D R A E D L

21ella - #695 TCCAAACCACA TCTGCTGGCT CTGGGGTCCC AGTGAATTCT GTGGCAAAAT ATATATTTTC ACTAACTCAA AAAAAAAA AAAAAA
21ella - #205 TCCAAACCACA TCTGCTGGCT CTGGGGTCCC AGTGAATTCT GTGGCAAAAT ATATATTTTC ACTAACTCAA AAAAAAAA AAAAAA

21ella - #2701 TCCAAACCACA TCTGCTGGCT CTGGGGTCCC AGTGAATTCT GTGGCAAAAT ATATATTTTC ACTAACTCAA AAAAAAAA AAAAAA
S N H T C W L W G F S E F W W Q I Y I P T N S K K K K K K

21ella - #295 AAAAAAAA AAAAAAAA

21ella - #2791 AAAAAAAA AAAAAAAA
K K K X K K

Exhibit C

BLASTP vs. PNU (AA) fib21ellorfas - 5:26:57 pm on Dec 21 98

BLASTP 1.4.10MP-WashU [30-Aug-96] [Build 20:24:58 Oct 21 1996]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Query= fib21ellorfas
(764 letters)

Database: /disk0/asap/databases/db/BRP/protxnu
345,099 sequences; 106,000,184 total letters.
.....done

Searching.....

	High Score	Smallest Sum Probability P(N)	Sum N
Sequences producing High-scoring Segment Pairs:			
GP:gi 2570933 (AF029310) vanilloid receptor subtype 1 [Rattus norvegicus]	336	1.9e-221	7
GP:gi 3986159 gnl PID d1035925 (AB015231) VR1sk [Mus musculus]	299	9.8e-136	6
GP:gi 2911863 (AF047660) contains similarity to ankyrin r...	103	6.5e-20	8
GP:gi 3675319 gnl PID e1344970 (Z74030) similar to ankyrin r...	97	1.1e-19	7
GP:gi 2642590 (AF031408) olfactory channel [Caenorhabditis elegans]	93	3.6e-16	6
GP:gi 2854148 (AF045639) contains similarity to ankyrin r...	93	4.1e-16	6
GP:gi 3879753 gnl PID e1349345 (Z72514) Similarity to Human...	73	3.6e-11	6
GP:gi 3267188 gnl PID e315126 (Y10601) ankyrin-like protein	71	2.7e-08	6
SP:SP:sp P48894 TRPL_DROME TRANSIENT-RECEPTOR-POTENTIAL L...	69	2.2e-05	4
GP:gi 1841966 (U65916) ankyrin [Rattus norvegicus]	72	5.6e-05	3

WARNING: Descriptions of 4 database sequences were not reported due to the limiting value of parameter V = 1.

>GP:gi|2570933 (AF029310) vanilloid receptor subtype 1 [Rattus norvegicus]
Length = 838

Score = 336 (156.0 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
Identities = 67/112 (59%), Positives = 84/112 (75%)

Query: 206 FYFGELPLSLAACTKQWDVVSVILLENPHQPAASLQATDSQGNTVILHALVMISDN... 265
FYFGELPLSLAACT C +V +LL+N QPA + A DS GNTVILHALV ++DN+ +N
Sbjct: 245 PYFGELPLSLAACTNQLAIVKELLQNSWPADISARDVGNTVILHALVEADNTVDNTKF 304

Query: 266 VTSMYDQLQAGARLCPTVQLEDIRNLQDLTPLKLAKEGKIEIFRHILORE 317
VTSMY+ +L GA+L PT++LE+I N + LTPL LAA GKI + +ILORE
Sbjct: 305 VTSMYNEILILGAKLHPTLKLPEITNRKGTLPLALASSGKIGVLAYILQRF 356

Score = 316 (166.7 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
Identities = 65/138 (47%), Positives = 93, 38 (67%)

Query: 66 ASQPDPNRFDRDRLFNAVSRGVVPEDLAGLFPEYLSKTSKYLTDSYEYTEGSTGKTCLMKAVL 125
A + P +DR +F+AV++ +L L +L +T K LTDSE+ + TGK+TCL+KA+L
Sbjct: 104 AGEKPERLYDRRSI?DAVAQSNQCELESLLJWPLQRSKKRLTDSEFKDPETGKTCLLKAML 163

Query: 126 NLKDGVNACILPLLQIDR?SGNFQPLVNAQCTDDYRGHSALHIAIEKRSLOQCVLLVEN 185
NL +G N I LL + R + + VNA TD YY+G +ALHIAIE+R++ V LLVEN
Sbjct: 166 NLHNCQNDTIALLOVARKTDSLKOFVNAS!TDSYYKGQTALHIAIEERRNMTLVTLVEN 223

Query: 186 GANVHARACGRFFQKGQG 203

GA+V A A G FF+K +G

Sbjct: 224 GADVQAANGDFEKKTKG 241

Score = 299 (138.8 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-321
Identities = 69/175 (39%), Positives = 94/175 (53%)

Query: 391 FFLN5LCNLTYMIFTAVAYHOPTLKKAPHLKAEVGNSMLLTGHILILLGGIYLLVGQL 450
F+ NF +YM IFTA AY++P LK VGT +TG IL + +

Sbjct: 434 FYFNFVYCLYMIIFTAAAYYRPVEGLFPYKLKNTVGDYFRVTGEILSVXXXXXXORG 493

Query: 451 WYFWRRHVFIIWISFIDSYFEILPLFQALLKPVSQLCFLATEWYLPLLVSALVLGWLNL 510
YF +R + F+DSY EILF Q+L VS VL F + Y+ +V +L +GW N+L

Sbjct: 494 QYFLQRPSLKSLSVDSYSEILPPVQSLF, VSVVLYFSQRKEYVASMVPSLAMGWTNML 553

Query: 511 YYTRGFQHTGTIVSVMIQKVILRDLRPLLILVFLPGPAVALVSLSQEAWRPEAP 565
YYTRGFQ GIV+VMT+K+ILRDL R A+V+L ++ P

Sbjct: 554 YYTRGFQQMGIYAVMIEKMLRDLCRXXXXXXXTAVVTLIEDGKNNSLP 602

Score = 281 (130.5 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
Identities = 54/95 (56%), Positives = 70/95 (73%)

Query: 586 GAQYRGILEASLEPLFKFTIGMELAFQFQLHFRGMVLLILAYVLLTYILLNMLIALME 645
G Y + LELPKFTIGM+L F E F+ + +LLAYV+LTYILLNMLIALM

Sbjct: 624 GNSYNSLYSTCLELFKFTIGMGLEPTENYDPKAVPIILLLAYVILTYILLNMLIALMG 683

Query: 646 ETVNNSVATDSWSIWKLQKAISVLEMENGYWWRK 680

ETVN +A +S +IWKLQ+AI++L+ E + C +K

Sbjct: 684 ETVNKIAQESKNIWKLQRAITILDTEKSFLKCMRK 718

Score = 162 (75.2 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
Identities = 28/38 (73%), Positives = 34/73 (89%)

Query: 323 HLSRKFTEWCYGPVRVSLYDLASVDSCCEENSVLEIIAP 360
HLSRKFTEW YGPV SLYDL +D+CE+NSVLE+IA+

Sbjct: 364 HLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIA 401

Score = 144 (66.9 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
Identities = 25/47 (53%), Positives = 31/47 (65%)

Query: 678 RKKQRAGVMTVGTKEPDGSPDERWCPRVVEVNWA\$WZOTLPTLCEDP 724
RK R+G +L VG PDG D RWCFRV+EVNW +W + + EDP

Sbjct: 717 RK3FRSGKILLOVGEYTDPDKDDYRWCFRVDEVNWTWNTNVGIINEDP 763

Score = 94 (43.6 bits), Expect = 1.9e-221, Sum P(7) = 1.9e-221
Identities = 15/30 (50%), Positives = 24/30 (80%)

Query: 363 KSPHRHRMVVLEPLNKLLQAKWDLLIPKFF 392
++P+RH M+++EPLN+LLQ KWD + + F

Sbjct: 405 ETPNRHDIMLLVEPLNRLQDKWDRFVKRIF 434

Score = 46 (21.4 bits), Expect = 1.3e-162 Sum P(6) = 1.3e-162
Identities = 11/48 (22%), Positives = 24/45 (50%)

Query: 435 HILLLGGIVLLVGQLWYFWRRHVFIIWISFIDSYFEILFLFCALLKPV 482
H ++L+ + L+ W + + +F+ + I+F A -PV

Sbjct: 410 HDMLLVPLNRLQDKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPV 457

Score = 37 (17.2 bits), Expect = 2.4e-169, Sum P(7) = 2.4e-169
Identities = 8/22 (36%), Positives = 13/22 (59%)

Query: 297 PLKLAKEGKIEIPRHIQRF 318
PL LAA + I + +LQ +

Sbjct: 251 PLSLAACTNQLAIVKFLLQNSW 272

Score = 37 (17.2 bits), Expect = 1.9e-111, Sum P(7) = 1.9e-111
Identities = 8/26 (30%), Positives = 15/26 (57%)

Query: 206 FYFGELPLSLAACTKQWDVVSYLLEN 231
 +Y G+ L +A + +V+ L+EN
Sbjct: 198 YYKGQTALHIAIERRNMTLVTLVEN 223

>GPB:gi|3926159|gnl|PID|d1035925 (AB015231) vrlsk [Mus musculus]
Length = 563

Score = 299 (138.8 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136
Identities = 69/175 (39%), Positives = 94/175 (53%)

Query: 391 FFLNFLCNLIVMPFIFTAVAYHQPTLKKAAPHILKAEVGNSMILLTCHILILLGGIYLLVGQL 450
 F+ NP +YM IFTA AY++P LK VG+ +TG IL + T
Sbjct: 127 FYFNFFVYCLYMIIFTAAAYVRVEGLPPYKLKNTVGDYPRTGEILSVXXXXXXRGIT 186

Query: 451 WYPWRRHVPWIWISPIDSYVPEILFLFQALLKPVSQVLQFLAIWYLPLLVSALVLGWLNL 510
 YF +R + P-DSV EILE Q+L VS VL F + Y+ +V +L +GW N+L
Sbjct: 187 QYFLQRPSLKSLSFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWITNML 246

Query: 511 YYTRGFQWTGIYSVMIQKVILRDLLRFLLIYLVFLFGFAVALVSLSQEAWRPEAP 565
 YYTRGFQ GIY+VMI+K+ILRDL R A+V+L + P
Sbjct: 247 YYTRGFQQMQIYAVMIEKMLRDLCRXXXXXOXXXXXXTAUVTLIEDGKNNSLP 301

Score = 253 (117.5 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136
Identities = 50/89 (56%), Positives = 64/89 (71%)

Query: 586 GAQYRGILEASLPLFKFTIGMGELAFQEQLMFRGMVLLLLAYVLLTYILLNNMLIALMS 645
 G Y + LEFLKFETIGMG+L P E F+ + +LLAYV+LTYILLNNMLIALM
Sbjct: 317 GNSYNNSLYSTCLELFKFTIGMDLEPTENYDFKAVFIILLAYVILTYILLNNMLIALMG 376

Query: 646 ETVNSVATDSWSIWKLQKAI SVLEMENGY 674
 ETV V+ -S IWXLQ A +L++E +
Sbjct: 377 ETVGQVSKESKHIIWKLQWATTILDIERSF 405

Score = 163 (75.7 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136
Identities = 28/47 (59%), Positives = 34/47 (72%)

Query: 678 RKKQRAGVMLTVGTPDGSPDERWCFRVEVNWASWEQTLPTLCEDP 724
 RK R+G M+TVG DG+PD KWCFRV+EVNW+ W Q L + EDP
Sbjct: 410 RKAFRSGEMVTVGKSSDGTTPDRRWCFRVEDVNWSHWNQNLGIINEDP 456

Score = 163 (75.2 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136
Identities = 28/38 (73%), Positives = 34/33 (89%)

Query: 323 HLSRKFTEWCYGDRVRSVSLYDLASVDSCEENSVLEIIAF 360
 HLSRKFTEW YGPV SLYDL+ +D+CE+NSVLE+IAT
Sbjct: 57 HLSRKFTEWAYGPVHSSLYDLSCIDTC2KNSVLEVIAY 94

Score = 129 (59.9 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136
Identities = 27/49 (55%), Positives = 36/49 (73%)

Query: 269 MYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAKEKGKIEIFRHILQRE 317
 MY+ +L GA+L PT++LE+I N + LTPL LAA GKI + +ILQRE
Sbjct: 1 MYNEBILILGAKLHPTLKLEEITNRKGLTPLALAASSGKIGVILAYILQRE 49

Score = 94 (63.6 bits), Expect = 9.8e-136, Sum P(6) = 9.8e-136
Identities = 15/30 (50%), Positives = 24/30 (80%)

Query: 363 KSPHRHRMVVLEPLNKLLQAKWDLLIPKFP 392

--P+RH M+++EPLN+LLQ KWD + + F
Sbjct: 98 ETPNRHDLLV2PLNRLLQEKWDRFVKRIT 127
Score = 46 (21.4 bits), Expect = 2.3e-77, Sum P(5) = 2.3e-77
Identities = 11/46 (22%), Positives = 24/45 (50%)

Query: 435 HILILLGGCIVLLVGQLWYFWRRHVPWIWISPIDSYPEIILFLFQALLKPV 482
H + + L + T + I + W + + + F + S + + I+F A + PV
Sbjct: 103 HIDMLLV2PLNRLLQDKWDRFVKRIFYENFPVYCLYMIIFTAAAYRPV 150
Score = 42 (19.5 bits), Expect = 1.2e-122, Sum P(6) = 1.2e-122
Identities = 9/22 (40%), Positives = 16/22 (72%)

Query: 209 GELPLSLAACTKQWDVVSYLLE 230
G PL-LAA + + V+ + Y+L+
Sbjct: 26 GLTPLALAAASSGKIGVULAYILQ 47

>GP:gi|2911863 (AF047660) contains similarity to ankyrin repeats
[Caenorhabditis elegans]
Length = 900

Score = 103 (47.8 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20
Identities = 23/89 (25%), Positives = 44/89 (49%)

Query: 497 LLVSALVLGWLNLYYTTRGFQHTGIVSVMQKVLIRDLRLFLIYLVLFLGFAVALVLS 556
L+ + + + LYY R + G + -M+ + I D+ RF+LTY +PL GF+ +
Sbjct: 592 LITVTMIFTTVHLYLYYCRVIRFVGPVFLMVYTIIATDIFRFMLIYGIPLMGFQSFSLIF 651

Query: 557 QEAWRPPEAPTGPNATESVQPMEGQEDEGN 585
R T+ + EG + + N
Sbjct: 652 LSCERSEANVIKKLITDQSEASEGSQNKFN 680

Score = 63 (29.3 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20
Identities = 15/37 (55%), Positives = 18/27 (66%)

Query: 291 NLQDLTPLKLAKEKGKIEIFRHILQRE 317
N Q L+PL LAAK K E+F IL+ E
Sbjct: 328 NKQSLSPLTIAAKLAKKEMFDEILELE 354

Score = 56 (26.0 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20
Identities = 16/48 (33%), Positives = 25/42 (52%)

Query: 151 LVNAQCTDDYYRGHSAHLIAIZKRSLOCVALLVENGANVHARACGRPP 158
L+N + + G S LH AI + V + + GA+V+ + R G FF
Sbjct: 185 LLNDIHT92DFYGLSPLRHOAIINTDCKLVYKFLKLGADVNSRCYGAFF 232

Score = 54 (25.1 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20
Identities = 12/25 (52%), Positives = 13/23 (56%)

Query: 207 YFGELPLSLAACTKQWDVVSYLL 229
Y GE PLS AAC Q + LL
Sbjct: 263 YLGEYPLSFAACLNQPESPRLLL 285

Score = 49 (22.8 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20
Identities = 8/23 (34%), Positives = 12/23 (52%)

Query: 331 WCYGPVRVSLYDILASVDSCRENS 353
W YG + Y LA -D+ E +
Sbjct: 359 WAYGDASSTAYPLAKIDTINETT 381

Score = 47 (21.8 bits), Expect = 6.5e-20, Sum P(8) = 6.5e-20
Identities = 11/30 (36%), Positives = 18/30 (60%)

Query: 236 ASLOATDSQENTVHLHALVMISDNESAENIAL 265
 A+ A D+ G+V+L+ V+ + + + AL
 Sbjct: 289 ANPNAQDTINGNSVLHMCVIHENMAMFKLAL 318

Score = 46 (21.4 bits). Expect = 5.7e-13. Sum P(6) = 5.7e-13
 Identities = 9/27 (33%). Positives = 17/27 (62%)

Query: 163 GHSALHIAIEKRSIQLCVKLLVENGANV 189
 G+S LH+ + + + KL +E GA+
 Sbjct: 298 GNSVLFMCMVIHENMAMFKLALBCGASL 324

Score = 43 (20.0 bits). Expect = 6.5e-20. Sum P(8) = 6.5e-20
 Identities = 8/18 (44%). Positives = 13/18 (72%)

Query: 634 ILLINMLIALMSETVNSV 651
 I+ NMLIA+M+ T +
 Sbjct: 753 IMQPNNMLIAMMTRTYETI 770

Score = 41 (19.0 bits). Expect = 6.5e-20. Sum P(8) = 6.5e-20
 Identities = 10/27 (37%). Positives = 16/27 (59%)

Query: 113 GSTGKTCLMKAVLNLDGVNACILFLL 139
 GS G-T + +L+ D NA +L +L
 Sbjct: 153 GSMGETIIGCCLLHASDIHNALVLKIL 179

Score = 35 (16.3 bits). Expect = 0.00016. Sum P(3) = 0.00016
 Identities = 9/37 (24%). Positives = 16/37 (43%)

Query: 67 SQFDPNRFDRLPDAV5RGVPEDLAGLPYVLSKTSK 103
 S-P P R+ + + V + GL E+ S+
 Sbjct: 464 SERPPGRYGKNSTLQQVKPVINATSRGLVEWSEPLSC 500

Score = 34 (15.8 bits). Expect = 6.8e-11. Sum P(8) = 5.6e-11
 Identities = 8/31 (25%). Positives = 17/31 (54%)

Query: 422 LKAEGVGNMSLLTGHIILLGGIYLLVGQLWY 452
 L + + + L+ + + LI + I+ V L-Y
 Sbjct: 577 LACDLSPVLLVVVDNVLITVTMIFTTVHYLY 607

>GP:gi|3875319|gnl|PID|el344970 (274030) similar to ankyrin repeats
 [Caenorhabditis elegans] >GP:gi|3876480|gnl|PID|el346172 (272508)
 similar to ankyrin repeats [Caenorhabditis elegans]
 Length = 790

Score = 97 (45.0 bits). Expect = 1.1e-19. Sum P(7) = 1.1e-19
 Identities = 18/53 (33%). Positives = 32/53 (60%)

Query: 497 LLVSALVLGWLNLVLYTRGFQHTGIYSVMIQKVILRDLIRFLLLYLVFLFGFA 549
 + + + + + L + LYY R G + + + I DL+RF +IY +FL GF+
 Sbjct: 526 MALLISILLVTOHQFLYYMRAIPFVGPFVLMVYTIIATDLVRFAMIYSIFLVGFS 578

Score = 89 (41.3 bits). Expect = 1.1e-19. Sum P(7) = 1.1e-19
 Identities = 19/48 (39%). Positives = 27/48 (56%)

Query: 151 LVNAQCTDDVYRGHSALHIAIEKRSIQLCVKLLVENGANVHARACGRFF 198
 L+N C + Y G S LH+AI + Q IL+ GA+ + R G FF
 Sbjct: 189 LINDICVSEYYGLSPLHLAJVNQDAQFTSILRLGADLNQRACYGAFB 236

Score = 62 (28.8 bits). Expect = 1.1e-19. Sum P(7) = 1.1e-19
 Identities = 13/23 (56%). Positives = 14/23 (60%)

Query: 207 YFGELPLSLAACTKQWDVVSYLL 229
YFGE PLS A C Q D+ LL
Sbjct: 267 YFGEYPLSPAICMGORHDLFRMLL 289

Score = 51 (23.7 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19
Identities = 10/19 (52%), Positives = 13/19 (68%)

Query: 236 ASLQATDSQGNTVLHALVM 254
A+L A D+ GNT LH V+
Sbjct: 293 ANLSAQDTNGNTALHLCVI 311

Score = 49 (22.6 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19
Identities = 11/51 (21%), Positives = 27/51 (52%)

Query: 601 KPTIGMGEЛАFQEQLHFRGMVLLLLAYVLLTIVILLNMLJALMSFTVNSV 651
+F+ + E++ + + L+ + + IL N+LIA+M+ T ++
Sbjct: 626 EFSVLYREMSACDFWMKWIGKLIFVIFET/\SILQFNLLIAMMRTTYETI 676

Score = 43 (20.0 bits), Expect = 1.2e-06, Sum P(5) = 1.2e-06
Identities = 7/27 (25%), Positives = 16/27 (59%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANV 189
G++ALK+ + + + + E G N+
Sbjct: 302 GNTALHLCVIHDKMDMLDAVLEAGGNT 328

Score = 39 (18.1 bits), Expect = 5.5e-12, Sum P(7) = 5.5e-12
Identities = 12/56 (21%), Positives = 25/56 (44%)

Query: 461 WISFIDSYFEILFLFQALLKPFVSQVLCPFLALEWYLPLLVSALVLGWLNLYYTRGF 516
W +F+ + + L A L + + C LA ++ L + + + + L T+ S
Sbjct: 483 WFNFLKAPPALMFKGABLFIIISIPCRILACSFHEFFLTIDNTMAIISILLVTQHF 538

Score = 38 (17.6 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19
Identities = 9/18 (50%), Positives = 12/18 (66%)

Query: 289 IRNLQDLITPLKLAKEGK 306
+ N Q+LT L LAAT K
Sbjct: 330 LANKQNLTLTAAARLAK 347

Score = 37 (17.2 bits), Expect = 4.7e-18, Sum P(7) = 4.7e-18
Identities = 7/15 (46%), Positives = 9/15 (60%)

Query: 723 DFSGAGVPRTELNPV 737
DF G+ +ENPV
Sbjct: 599 DPMGSEPNINMENPV 613

Score = 36 (16.7 bits), Expect = 1.1e-19, Sum P(7) = 1.1e-19
Identities = 10/47 (21%), Positives = 16/47 (34%)

Query: 376 LNKLLQAKWDLIIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKAAPH 422
+ +L KW +L L I+ + AY HL
Sbjct: 362 IEQILDEWKAYGRALWRSLLGFIFYCCFCVCAYMRLPSSATTEHL 408

Score = 35 (16.3 bits), Expect = 3.0e-08, Sum P(6) = 3.0e-08
Identities = 9/23 (39%), Positives = 11/23 (47%)

Query: 207 YFGELPLSLAACTKQWDVVSYLL 229
Y+G PL LA + S LL
Sbjct: 199 YYGLSPHLAIVNQDAQFTSLLL 221

Score = 34 (15.8 bits), Expect = 3.9e-12, Sum P(5) = 3.9e-12
Identities = 7/21 (33%), Positives = 13/21 (61%)

Query: 297 PLKLAKEKGKIEIFRHILQRE 317
PL A G+ +FR +L ++
Sbjct: 272 PLSFAICMEQHDLPRMLLAKK 292

Score = 34 (15.8 bits), Expect = 8.9e-10, Sum P(7) = 8.9e-10
Identities = 6/18 (33%), Positives = 12/18 (66%)

Query: 610 AEQEQLNFRGMVLLLLA 627
AF +L F+G L +++
Sbjct: 489 AFAKLMFKGAPLFIIIS 506

Score = 34 (15.8 bits), Expect = 4.0e-08, Sum P(6) = 4.0e-08
Identities = 11/40 (27%), Positives = 16/40 (40%)

Query: 153 NAQCTDDYYRGHSALHIAIEKRSLQCVKLIVENGANVHAR 192
N T Y G L AI +L+ AN+ A+
Sbjct: 259 NTNYTGSMYFGEYPLSPAICMGQHDLPRMLLAKKANLSRQ 298

>GP:gi|2642590 (AF031408) olfactory channel [Caenorhabditis elegans]
Length = 937

Score = 93 (43.2 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16
Identities = 19/36 (52%), Positives = 25/36 (69%)

Query: 163 CHSALHIAIEKRSLQCVKLIVENGANVHARACGRFF 198
G SALH+AI + V LL+ + A+V+ARACG FF
Sbjct: 172 GQSALHIAIVHDDYPTVSSLNLNSKADVNARACGNFF 207

Score = 92 (42.7 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16
Identities = 20/53 (37%), Positives = 31/53 (58%)

Query: 497 LLVSALVLGWLNLLYYTRGFQHTGIYSVMICKVILRDLLRPLLIVLVFLFGFA 549
L V AL W+ LL+ R + TG + MI +I D+RF +J +FL F+
Sbjct: 500 LFVBALPGSWIFLFBARSALKTGFVQMTYSMIAGDMIRFAIIASAIFLVSFS 552

Score = 57 (26.5 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16
Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 207 YFGELPLSLAACTKQWDVVSYLLE 230
Y+GE BL+ AAC D+ L++
Sbjct: 226 YYGEYPLAFAACPGNKDIYDILLIQ 249

Score = 50 (23.2 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16
Identities = 11/25 (44%), Positives = 15/25 (60%)

Query: 291 NLQDLTPLKLAKEKGKIEIPRHILQ 315
N TPL LA K G+ +IF +L+
Sbjct: 294 NHAGFTPLTLATKLGRKQIFEFMLE 318

Score = 44 (20.4 bits), Expect = 6.8e-16, Sum P(5) = 6.8e-16
Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 242 DSQGNTVILHALVMISNSAENIAL 265
DS GNT+LH V+ +S + A+
Sbjct: 258 DSPGNNTILHMCVINYSSSMYSYAV 281

Score = 37 (17.2 bits), Expect = 2.2e-05, Sum P(4) = 2.2e-05
Identities = 9/24 (37%), Positives = 13/24 (54%)

Query: 208 PGELPLSLAACTKQWDVVSYLLEN 231
PG+ L LA ++ VS LL +
Sbjct: 171 FGQSALHIAIVHDDYETVSSLNLNS 194

Score = 34 (15.8 bits), Expect = 3.6e-16, Sum P(6) = 3.6e-16
Identities = 7/21 (33%), Positives = 11/21 (52%)

Query: 364 SPHRHMRMVVLREPLNKLQAKW 384
+P M+ E + +LL KW
Sbjct: 363 TPEHLDMIGSEVIQRILLADKW 383

>GP:gi|2854148 (AF045639) contains similarity to ankyrin repeats
[Caenorhabditis elegans]
Length = 957

Score = 93 (43.2 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16
Identities = 19/36 (52%), Positives = 25/36 (69%)

Query: 163 GHSALHIAIEKRSLOCVKLLVENGANVHARACGRRF 196
G SALH+AI + V LL+ + A-V+ARACG FP
Sbjct: 175 GQSALHIAIVHDDYETVSLLLNSKADVHARACGNFF 210

Score = 92 (42.7 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16
Identities = 20/53 (37%), Positives = 31/53 (58%)

Query: 497 LLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVPLFGFA 549
L V AL W+ LL++ R + TG + MI +I D+ RF +I -FL P+
Sbjct: 503 LFVPALPGSWIFLLFFARSALKTGPFVQMIYSMIAQDMIRPAIIISAIPLVSPS 555

Score = 57 (26.5 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16
Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 207 YFGELPLSLAACTKQWDVVSYLLE 230
Y+GE PL+ AAC D+ L++
Sbjct: 229 YYGEYPLAFAACFGNKDIYDILLIQ 252

Score = 50 (23.2 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16
Identities = 11/25 (44%), Positives = 15/25 (60%)

Query: 291 NLQDLTSLKLAKEGKIEIPRHLIQ 315
N TPL LA K G+ +IF +L+
Sbjct: 297 NHAGFTPLTLATKLGRKQIFPEEMLE 321

Score = 44 (20.4 bits), Expect = 7.6e-16, Sum P(5) = 7.6e-16
Identities = 10/24 (41%), Positives = 15/24 (62%)

Query: 242 DSQGNITVLHALVMISDNSAENIAL 265
DS GNT+LH V+ -S + AT
Sbjct: 261 DSFGNTILHMCVINYSSSMYSYAV 284

Score = 37 (17.2 bits), Expect = 2.4e-05, Sum P(4) = 2.4e-05
Identities = 9/24 (37%), Positives = 13/24 (54%)

Query: 208 FGELPLSLAACTKQWDVVSYLLEN 231
FG+ L LA ++ VS LL +
Sbjct: 174 FGQSALHIAIVHDDYETVSLLLNS 197

Score = 34 (15.8 bits), Expect = 4.1e-16, Sum P(6) = 4.1e-16
Identities = 7/21 (33%), Positives = 11/21 (52%)

Query: 364 SPHRHMRMVVLREPLNKLQAKW 384
+P M+ E + +LL KW
Sbjct: 366 TPEHLDMIGSEVIQRILLADKW 386

>GP:gi|3879753|gnl|PID|e1349345 (272514) Similarity to Human ankyrin
(SW:ANK1_HUMAN) [Caenorhabditis elegans]
Length = 519

Score = 73 (33.9 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 17/36 (47%), Positives = 19/36 (52%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANVHARACGRFF 198
C S LH AI L+ V L GA+VH R G FF
Sbjct: 186 GLSPLHQAIVNEDLENVYFLCRKGADVHQRCYGSF 221

Score = 63 (29.3 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 12/17 (70%), Positives = 13/17 (76%)

Query: 207 YFGELPLSLAACTKQWD 223
Y+GE PLS AACT Q D
Sbjct: 252 YWGHYPLSFAACTNQVD 268

Score = 52 (24.1 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 13/27 (48%), Positives = 17/27 (62%)

Query: 289 IRNLQDLTPLKLAKEGKIEIFRHILC 315
+RN LTPL LAAT K I+ IL+
Sbjct: 315 VRNNLKLTPPLALAARLAKKHIYDYLILE 341

Score = 51 (23.7 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 10/22 (45%), Positives = 12/22 (54%)

Query: 331 WCYGPVRVSLYDLASVDSCREEN 352
W YGPV Y L VD+ E+
Sbjct: 348 WRYGPVVCKAYPLNDVDTINES 369

Score = 43 (20.0 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 8/13 (61%), Positives = 10/13 (76%)

Query: 242 DSQGNTVLHALVM 254
D+ GNTVLH V+
Sbjct: 284 DTNGNTVLHLTVI 296

Score = 37 (17.2 bits), Expect = 3.6e-11, Sum P(6) = 3.6e-11
Identities = 8/35 (22%), Positives = 16/35 (45%)

Query: 376 LNKKLCAKWDLLIPKFBINFLCNLIYMFIFT>VAY 410
+ + + L++KW+ K L IV +A+
Sbjct: 398 IEEVLESKWETPGKKQLPMSLAGYIVPLAVFYLA 432

>GP:gi|3287188|gnl|PID|e315126 (Y10601) ankyrin-like protein [Homo sapiens]
Length = 1119

Score = 71 (33.0 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08
Identities = 13/30 (43%), Positives = 20/30 (66%)

Query: 163 GHSALHIAIEKRSLQCVKLLVENGANVHAR 192
G++ LH A+EK ++ VK L+ GAN + R
Sbjct: 98 GNTPLHCAVEKNQIESVKFLLSRGANPNLR 127

Score = 63 (29.3 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08
Identities = 10/30 (33%), Positives = 20/30 (66%)

Query: 501 ALVLGWLNLLVYTRGFQHTCIYSVMIQKVI 530
A+ W+N L Y + F++ GI+ VM++ ++
Sbjct: 638 AVYPYWMMNLLYLQRPENCGIFIVMLEVIL 867

Score = 59 (27.4 bits), Expect = 9.0e-07, Sum P(6) = 9.0e-07
Identities = 10/30 (33%), Positives = 19/30 (63%)

Query: 167 LHIAIEKR5LQCVKLLVENGANVHARACGR 196
LH+A++ L+ +K+ +NGA + GR
Sbjct: 243 LHLAVONGDLEMIRNCMLDNGAQIDPVEKGR 272

Score = 50 (23.3 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08
Identities = 10/26 (38%), Positives = 18/26 (69%)

Query: 291 NLQDLTPLKLAKEGKIEIFRHILQR 316
+L +TFL LAAK G + + +L++
Sbjct: 479 DLHGMTPLHLAAKNGHDKVVQLLLKK 504

Score = 49 (22.8 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08
Identities = 10/26 (38%), Positives = 14/26 (53%)

Query: 209 GELPLSLAACTKQWDVVSYLLENPHQ 234
G PL LA + W++V+ LL Q
Sbjct: 342 GRSPLILATASASWNIUNLLSKGAQ 367

Score = 48 (22.3 bits), Expect = 3.2e-05, Sum P(5) = 3.2e-05
Identities = 9/32 (28%), Positives = 20/32 (62%)

Query: 524 VMIQKVILRDLLRFLLIYLVFLFGFAVALVS.. 555
+ + + +VIL+ LLR + + + + L F + +
Sbjct: 860 IVMLEVILKTLLRSTVVPIFLLLAPGLSFYIL 891

Score = 41 (19.0 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08
Identities = 9/28 (32%), Positives = 15/28 (53%)

Query: 525 MIQKVILRDLLRFLLIYLVFLFGFAVAL 552
+I K +LR + F + + L F F + L
Sbjct: 865 VILKTLLRSTVVPIFLLLAPGLSFYILL 892

Score = 40 (18.6 bits), Expect = 2.9e-07, Sum P(5) = 2.9e-07
Identities = 13/50 (26%), Positives = 24/50 (48%)

Query: 620 MVLLLLAYVLLTVILLNMLIALMSETVNSVATDSWSIWKLQKAISVLE 665
+V + LL + L + + +LLN+ S + + + T S + + S LE
Sbjct: 875 VVFIFLLLAPGLSFYILLNLQDPBSSPLLSIIQTFSSMCLGDINYRESFLE 924

Score = 40 (18.6 bits), Expect = 7.6e-05, Sum P(5) = 7.6e-05
Identities = 8/19 (42%), Positives = 12/19 (63%)

Query: 296 TPLKLAKEGKIEIFRHIL 314
TP+ LA + G +E+ + L
Sbjct: 241 TPLHLAVONGDLEMIRNCML 259

Score = 39 (18.1 bits), Expect = 2.7e-08, Sum P(6) = 2.7e-08
Identities = 7/19 (36%), Positives = 14/19 (73%)

Query: 625 LLAYVLLTVILLNMLIAL 643
L-++ + I+L+N+LI L
Sbjct: 941 LV\$FTIPVPIVLMNLLIGL 959

Score = 39 (18.1 bits), Expect = 6.8e-07, Sum P(6) = 6.8e-07
Identities = 9/36 (25%), Positives = 18/36 (50%)

Query: 293 QDLTPLKLAKEGKIEIFRHILQRRFSGLSHLSRKF 328
+ LF L + +IE+ H + +E+ + J+ F
Sbjct: 681 EPLTALNAMVQNYRIELLNHPVCKEYLLMKWLAYGF 716

Exhibit D**Qualified Target Summary Sheet**

Vanilloid Receptor Homologue (VR-2)	
CFA Disease Area(s):	Pain
Druggable Target Class:	Calcium channel
MPI Gene Sequence Identifier:	Fib2le11 (Mme 18560)
Top Blast Hit:	Rat vanilloid receptor 1 (VR1)
Amino Acid Coding Region:	ORF: 361-2652
cDNA Length:	2806 bp
Source (Tissue / Cell Line):	First clone identified in an internal heart library
Novel / Unrecognized:	? Unrecognized / Novel
% Novelty:	66% novel across the complete cDNA. Hits unannotated sequence in Non-Public Patent Data Base
Patent Status:	Filed Nov. 1, 1998
Full Length Clone:	Yes
Expression Profiling Results:	Present in a sub-population of sensory neurons different from VR1. Also present in sympathetic neurons.
Background:	The published vanilloid receptor (Caterina et. Al. Nature 389:816-24, 1997) responds to heat and capsaicin by activating Ca++ influx in sensory neurons (Tominaga et.al., Neuron 21: 531-43, 1998). Capsaicin also binds to this channel.
Hypothesis:	This channel may be responsible for hypersensitivity in chronic neuropathic pain and represents a unique target for pain.
Assay Type:	Cell-based assay
Reagents Needed:	Open reading frame will be cloned by Millennium into pCDNA 3.1
Readout:	
Critical Experiments Necessary:	

MPI Target Name:	Vanilloid Receptor Homologue (VR-2)
QT Nomination Date:	12/22/98
Action Taken:	Accepted QT (unrecognized) Pending full length cDNA
Date Accepted:	
Bayer QT Leader:	Rory Curtis or Peter DiStefano
MPI QT Leader:	

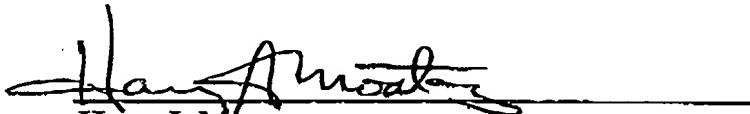
**BEFORE THE OFFICE OF ENROLLMENT AND DISCIPLINE
UNITED STATE PATENT AND TRADEMARK OFFICE**

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Expires: August 5, 2003



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